

Probabilistic mapping of human functional brain networks identifies regions of high inter-subject consensus

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Introduction

- Functional network organization can vary across individuals, obscuring the interpretation of group-average data. Thus, an important question for group analyses is which regions show the highest consensus network description across individuals.
- We can leverage information on both group consensus and individual specificity by taking a probabilistic approach to mapping networks in individuals.
- Here, we produce a probabilistic representation of 14 canonical brain networks.
- The goal is to provide a map of both high- and low-probability regions along with a set of ROIs that show high group consensus within each network.

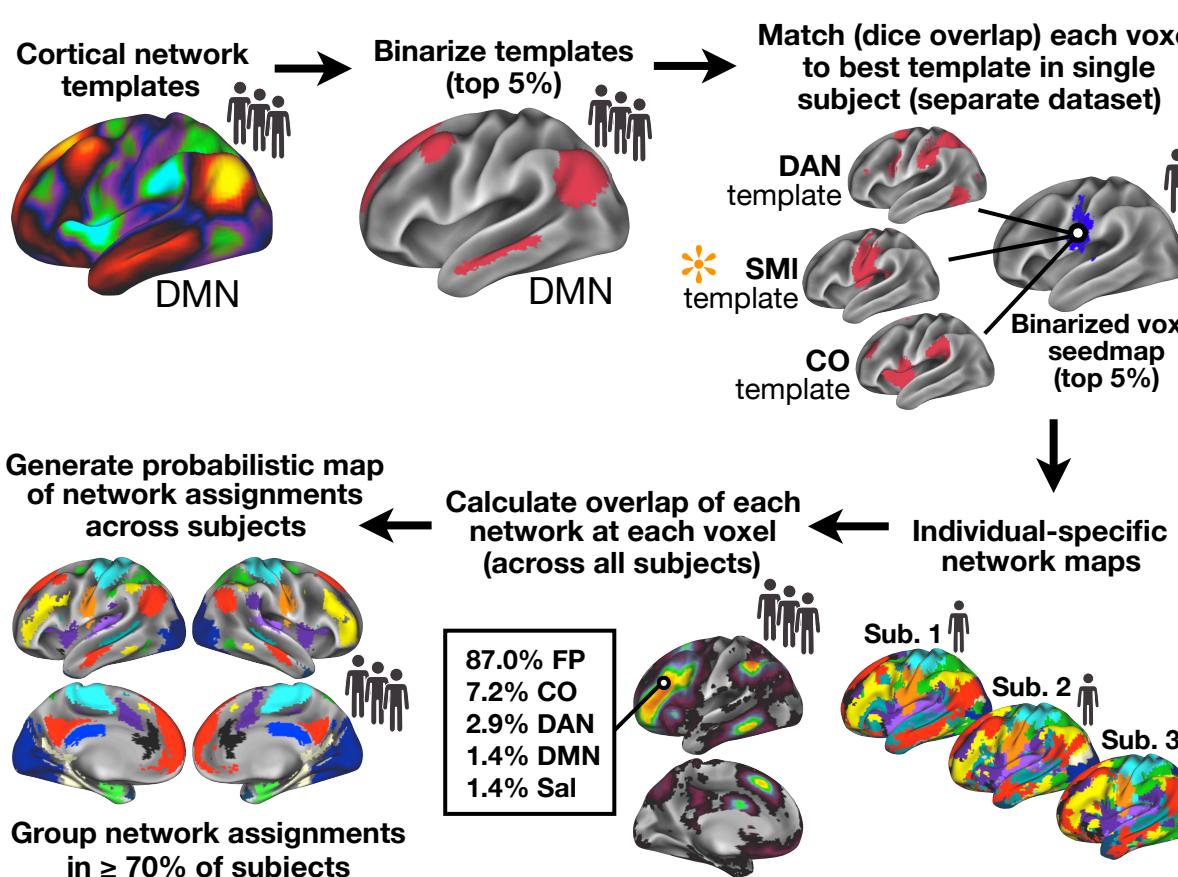
Methods

Dataset 1: WashU (N=24), 35+ min. rest data per subject, used for creation of network templates

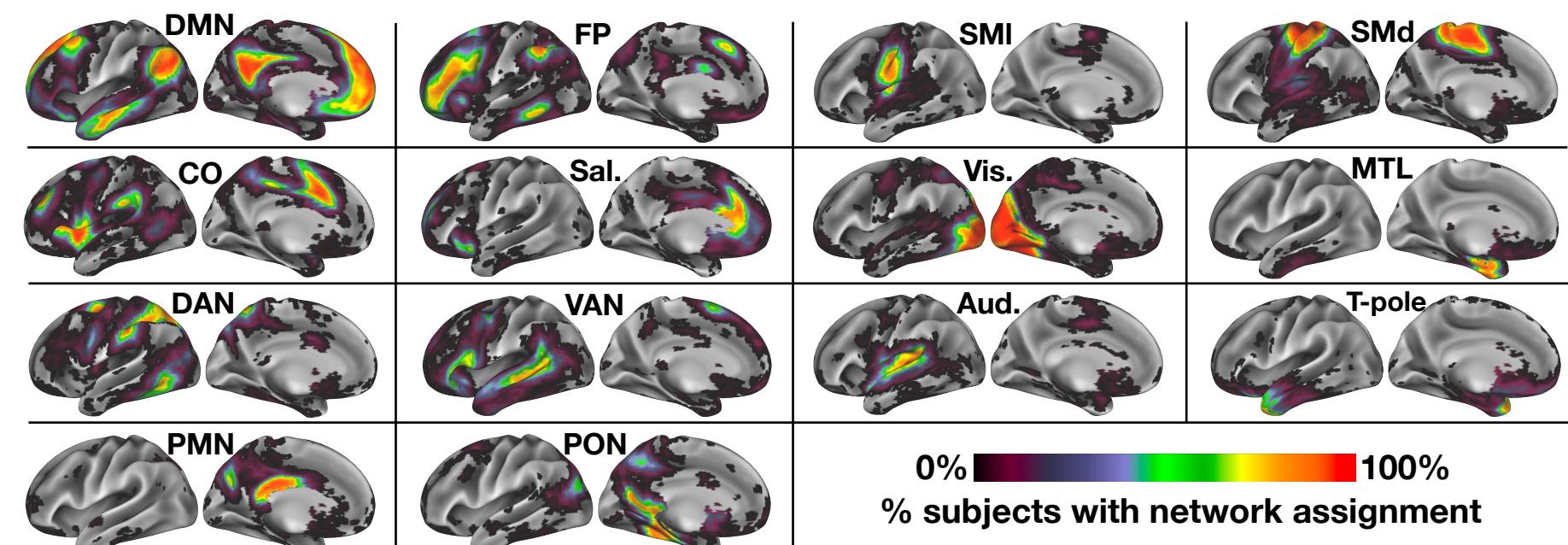
Dataset 2: Dartmouth (N=69), 20+ min. rest data per subject, primary dataset for probabilistic network mapping

Dataset 3: MSC (N=9), 5 hrs. rest data per subject, secondary dataset for probabilistic network mapping

Dataset 4: HCP (N=99), 52.5+ min. rest data per subject, secondary dataset for probabilistic network mapping

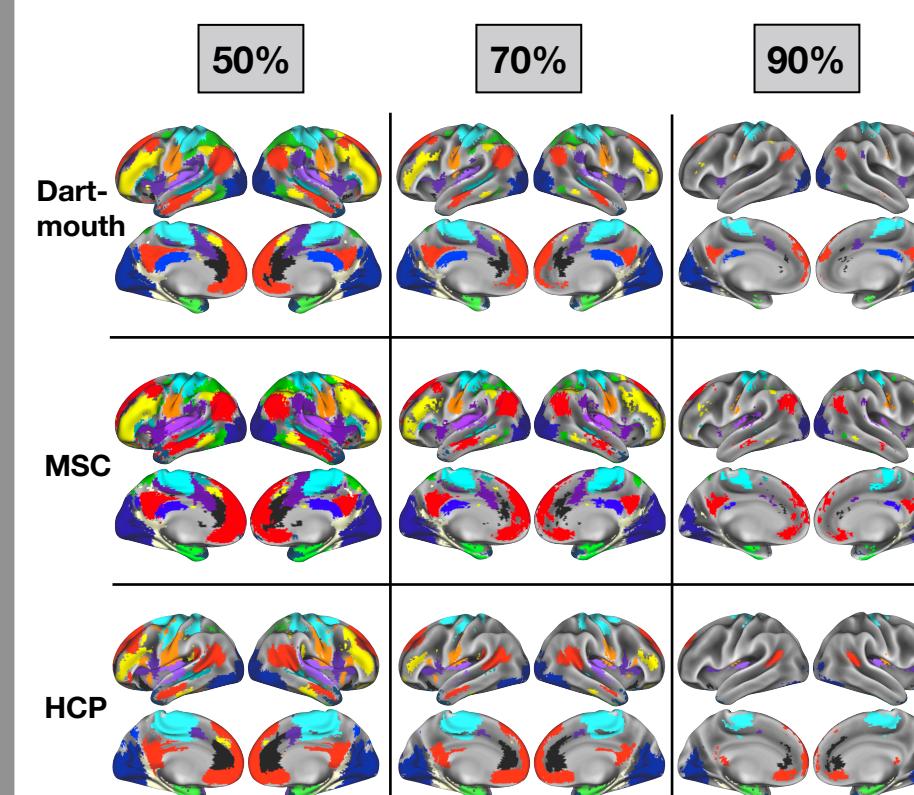


1. All networks have high-probability regions; peak probabilities vary by network

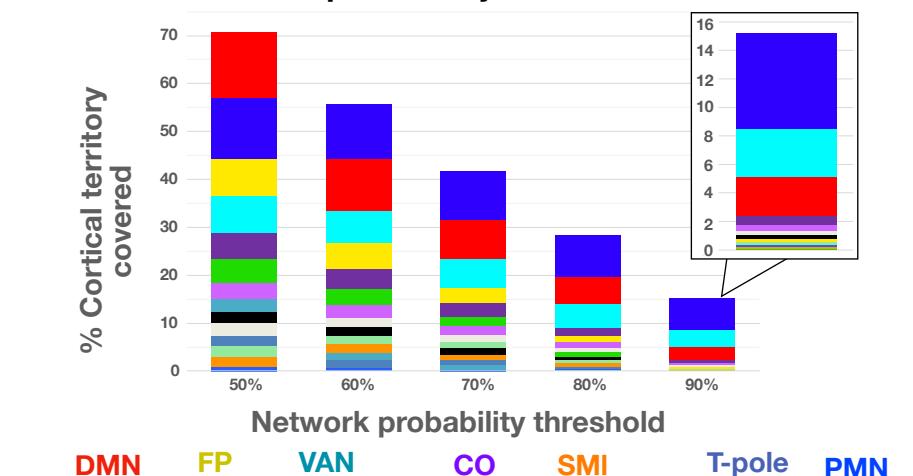


2. Core high-probability regions replicate across datasets; probabilistic cortical territory covered varies by network

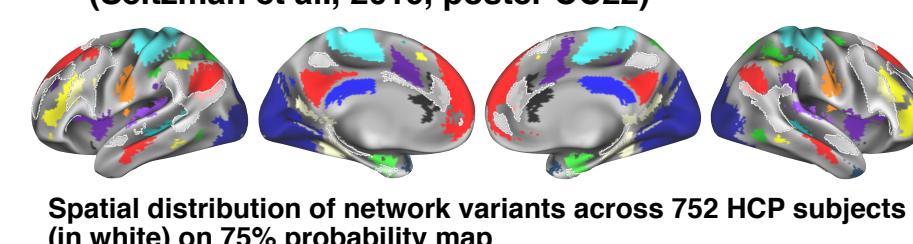
A) Distribution of high-probability regions is preserved across datasets



B) Some networks retain more cortical territory than others as probability threshold increases

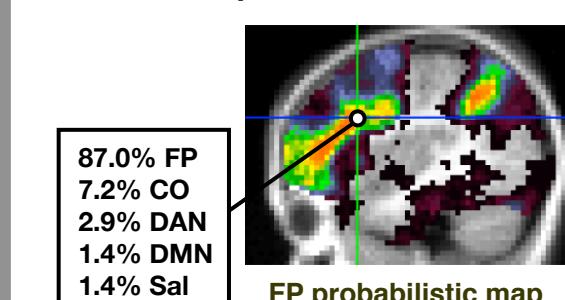


C) Low-probability regions relate to previous findings on the distribution of network variants (Seitzman et al., 2019, poster CC22)

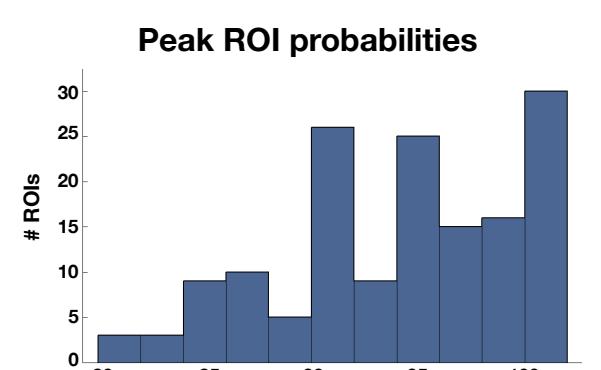
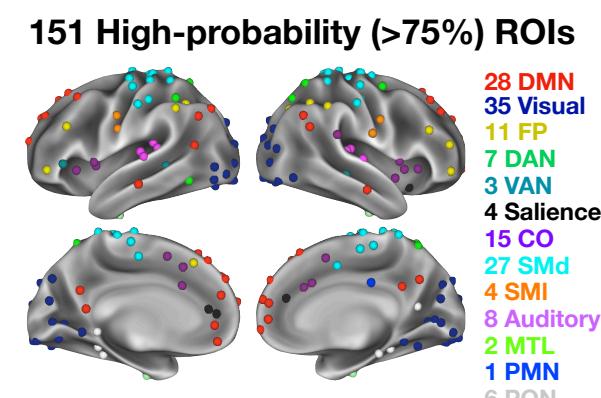
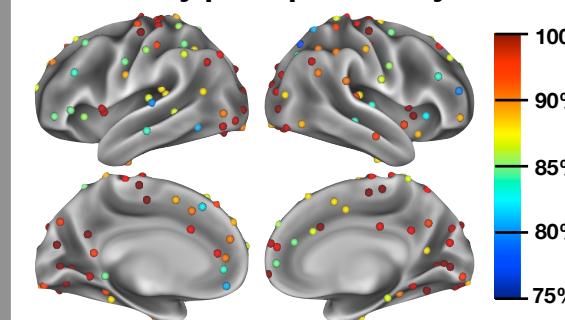


3. Voxelwise probability tools and network-specific ROIs were derived from probabilistic maps

Voxelwise point-and-click tool



ROIs by peak probability



High-probability ROIs (7 mm. diam.) were generated from a subset of the Power 264 ROIs (Power et al., 2011) within 3 mm. (1 voxel) of a high-probability (>75%) region (averaged across voxels within the ROI)

Scan this QR code or visit <https://github.com/GrattonLab> to download the ROI set and point-and-click tools.



Conclusions

- A probabilistic representation of functional networks produces regions of both high group consensus and high inter-subject variability for all networks
- Individual networks differ in the peak probability of their core regions, and in territory dropout across probability thresholds
- 151 high-consensus ROIs are produced from the probabilistic maps for research use in network-informed analyses

Acknowledgements and References

- This work was supported by the National Institutes of Health Grant R01MH118370 and the James S. McDonnell Foundation.
- Gordon et al., 2017. Individual variability of the system-level organization of the human brain. *Cerebral Cortex*
 - Power et al., 2011. Functional network organization of the human brain. *Neuron*
 - Seitzman et al., 2019. Trait-like variants in human functional brain networks. *PNAS*
 - Mueller et al., 2013. Individual variability in functional connectivity architecture of the human brain. *Neuron*